

1/141

## SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA  
PHARMALOGICALS RESEARCH PTE., LTD.

<120> ANTIBODIES AGAINST LESIONAL TISSUES

<130> C1-A0230P

<140> JP 2002-339241

<141> 2002-11-22

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<151> 2002-11-22

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<170> PatentIn version 3.1

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tca gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc 96  
Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe

2 / 1 4 1

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tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg			144
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met			
35	40	45	
gga tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt			192
Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe			
50	55	60	
cag gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac			240
Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr			
65	70	75	80
atg gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt			288
Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
gcg aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa			336
Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln			
100	105	110	
ggg cca atg gtc acc gtc tct tca			360
Gly Pro Met Val Thr Val Ser Ser			
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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

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3 / 1 4 1

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20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe  
50 55 60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr  
65 70 75 80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
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Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln  
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Gly Pro Met Val Thr Val Ser Ser  
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4 / 1 4 1

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 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn  
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ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144  
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

gca gtt ata tgg tat gat gga agt aat aaa tac tat gca gac tcc gtg 192  
 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac aca ctg tat 240  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

gcg aga gat cac ggc ctt ggt gat caa gcc tcc tgg ttc gac ccc tgg 336  
 Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp  
 100 105 110

ggc cag gga acc ctg gtc acc gtc tcc tca 366  
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp  
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn	
20                      25                      30	
ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg	144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35                      40                      45	
gca gtt ata tgg tat gat gga agt aat aaa tac tat gca gac tcc gtg	192
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val	
50                      55                      60	
aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac aca ctg tat	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65                      70                      75                      80	
ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85                      90                      95	
gcg aga gat cac ggc ctt ggt gat caa gcc tcc tgg ttc gac ccc tgg	336
Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp	
100                      105                      110	
ggc cag gga acc ctg gtc acc gtc tcc tca	366
Gly Gln Gly Thr Leu Val Thr Val Ser Ser	
115                      120	

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7 / 1 4 1

<213> Homo sapiens

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Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
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Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp  
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
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aca gtg aca atc tcc tgc aag gtt tct gga cac aac ttc atc gac cac 96  
Thr Val Thr Ile Ser Cys Lys Val Ser Gly His Asn Phe Ile Asp His  
20 25 30

tac atg cat tgg gta caa cag gcc cct gga aaa ggg ctt gac tgg atg 144  
 Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Asp Trp Met  
 35 40 45

gga cta att gac cct gaa gat ggt cag acg aaa tat tca gag agg ttt 192  
Gly Leu Ile Asp Pro Glu Asp Gly Gln Thr Lys Tyr Ser Glu Arg Phe  
50 55 60

gag ggc aga gtc aca att acc gcg gac aag tca aca gac aca acc tac 240  
Glu Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asp Thr Thr Tyr  
65 70 75 80

ttg gag gtg agc ggc ctg aga tcg gaa gac acg gcc gtt tat ttc tgt 288  
Leu Glu Val Ser Gly Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys  
85 90 95

aca acg gac ttg ggt gac ttg aat tat tgg aac cct ggt cac cgt ctc 336  
 Thr Thr Asp Leu Gly Asp Leu Asn Tyr Trp Asn Pro Gly His Arg Leu  
 100 105 110

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Leu	



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Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Asp Trp Met  
35 40 45  
Gly Leu Ile Asp Pro Glu Asp Gly Gln Thr Lys Tyr Ser Glu Arg Phe  
50 55 60  
Glu Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asp Thr Thr Tyr  
65 70 75 80  
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Leu

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn  
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

gca gtt ata tgg tat gat gga agt aat aaa tac tat gca gac tcc gtg 192  
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac aca ctg tat 240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

gcg aga gat cac ggc ctt ggt gat caa gcc tcc tgg ttc gac ccc tgg 336  
Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp  
100 105 110

ggc cag gga acc ctg gtc acc gtc tcc tca 366  
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Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn

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25

30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

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95

Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp

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Gly Gln Gly Thr Leu Val Thr Val Ser Ser

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tct ctg aag atc tcc tgt cag ggt tct gga tac aca ttt agc aat tac 96  
Ser Leu Lys Ile Ser Cys Gln Gly Ser Gly Tyr Thr Phe Ser Asn Tyr  
20 25 30

tgg atc gcc tgg gtg cgc cag agg ccc ggg aaa ggc ctg gag tgg atg 144  
Trp Ile Ala Trp Val Arg Gln Arg Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

ggg atc atc tat cct ggt gac tct gat atc aaa tac agt ccg tcc ttc 192  
Gly Ile Ile Tyr Pro Gly Asp Ser Asp Ile Lys Tyr Ser Pro Ser Phe  
50 55 60

caa ggc cat gtc acc atc tca gcc gac acg tcc atg aac acc gcc tac 240  
Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser Met Asn Thr Ala Tyr  
65 70 75 80

ctg cag tgg aac acc ctg aag gcc tcg gac acc gcc atg tac tac tgt 288  
Leu Gln Trp Asn Thr Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

gcg aga cat aaa ggg acc agg ttc ggg gag gtt ttg gcg gtt ggc aac 336  
Ala Arg His Lys Gly Thr Arg Phe Gly Glu Val Leu Ala Val Gly Asn  
100 105 110

1 3 / 1 4 1

tgg ttc gac ccc tgg ggc cag gga acc ctg gtc acc gtc tcc tca 381  
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20 25 30

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35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Ile Lys Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser Met Asn Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Asn Thr Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg His Lys Gly Thr Arg Phe Gly Glu Val Leu Ala Val Gly Asn  
100 105 110

Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120 125

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tcg gtg aaa ttc tcc tgc aag gct tcc gga ggc agc ttc agc aac tat 96  
Ser Val Lys Phe Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Asn Tyr  
20 25 30

gct atc acc tgg gtg cga cag gcc cct gga caa ggt ctt gag tgg atg 144  
Ala Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

gga agg atc atc cct atc ttt ggt ata cca aac tac gca cag gaa ttc 192  
Gly Arg Ile Ile Pro Ile Phe Gly Ile Pro Asn Tyr Ala Gln Glu Phe  
50 55 60

cag ggc aga gtc acg att acc gcc gac gat tcc acg acc aca gtc tac 240  
Gln Gly Arg Val Thr Ile Thr Ala Asp Asp Ser Thr Thr Thr Val Tyr  
65 70 75 80

atg gaa ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt 288  
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

1 5 / 1 4 1

gcg aga gat aat tca ata gga gca cct gat act tgg tgg ttc gac ccc 336  
Ala Arg Asp Asn Ser Ile Gly Ala Pro Asp Thr Trp Trp Phe Asp Pro  
100 105 110

tgg ggc cag gga cca cgg tca ccg tct cct ca 368  
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35 40 45

Gly Arg Ile Ile Pro Ile Phe Gly Ile Pro Asn Tyr Ala Gln Glu Phe  
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Asp Ser Thr Thr Thr Val Tyr  
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
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Ala Arg Asp Asn Ser Ile Gly Ala Pro Asp Thr Trp Trp Phe Asp Pro  
100 105 110

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Trp Gly Gln Gly Pro Arg Ser Pro Ser Pro

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tca gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc 96  
Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe  
20 25 30

tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144  
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

gga tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt 192  
Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe  
50 55 60

cag gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac 240  
Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr  
65 70 75 80

atg gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt 288



1 7 / 1 4 1

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85

90

95

gcg aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa 336

Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln

100

105

110

ggg aca atg gtc acc gtc tct tca

360

Gly Thr Met Val Thr Val Ser Ser

115

120

<210> 16

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20

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30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe

50

55

60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr

65

70

75

80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys

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95

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Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln  
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Gly Thr Met Val Thr Val Ser Ser  
115 120

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tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc aat 96  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn  
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

gca gtt ata tgg tat gat gga agt aat aaa tac tat gca gac tcc gtg 192  
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac aca ctg tat 240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

1 9 / 1 4 1

65                      70                      75                      80  
ctg caa atg aac agc ctg agg gcc gag gac acg gct gtg tat tac tgt      288  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                    85                      90                      95

gcg aga gat cac ggc ctt ggt gat caa gcc tcc tgg ttc gac ccc tgg      336  
Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp  
                    100                      105                      110

ggc cag gga acc ctg gtc acc gtc tcc tc      365  
Gly Gln Gly Thr Leu Val Thr Val Ser  
                    115                      120

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                    20                      25                      30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                    35                      40                      45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
                    50                      55                      60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65                      70                      75                      80

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
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Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp  
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser  
115 120

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20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

gca gtt ata tgg tat gat gga agc tat aaa tac tat gca gaa tcc gtg 192  
Ala Val Ile Trp Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Glu Ser Val  
50 55 60

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aag ggc cga ttc atc atc tcc aga gac aat tcc aag aac acc ctg tat 240  
 Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtc tat tac tgt 288  
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 85 90 95

gcg aga gat cgg ggg tcg gtg gag atg gct aca atc gcg gac tac tgg 336  
 Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp  
 100 105 110

ggc cag gga acc ctg gtc acc gtc tcc tca 366  
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 115 120

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 <213> Homo sapiens

<400> 20  
 Gln Val Gln Leu Ala Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr  
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Glu Ser Val  
 50 55 60

2 2 / 1 4 1

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp  
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 21

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (366)

<223>

<400> 21

cag gtc cag ctg gtg caa tct ggg gga ggc gtg gtc cag cct ggg agg 48  
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc agc ttc agt agc tat 96  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr  
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

2 3 / 1 4 1

gca gtt ata tgg tat gat gga agt tat aaa tac tat gca gaa tcc gtg 192  
Ala Val Ile Trp Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Glu Ser Val  
50 55 60

aag ggc cga ttc atc atc tcc aga gac aat tcc aag aac acc ctg tat 240  
Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

gcg aga gat cgg ggg tcg gta gag atg gct aca atc gcg gac tac tgg 336  
Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp  
100 105 110

ggc cag gga acc ctg gtc acc gtc tcc tca 366  
Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 22

<211> 122

<212> PRT

<213> Homo sapiens

<400> 22

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

2 4 / 1 4 1

Ala Val Ile Trp Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp

100

105

110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 23

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (366)

<223>

<400> 23

cag gtc cag ctg gtg caa tct ggg gga ggc gtg gtc cag cct ggg agg

48

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc agc ttc agt agc tat

96

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr

20

25

30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg

144



2 5 / 1 4 1

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

gca gtt ata tgg tat gat gga agt tat aaa tac tat gca gaa tcc gtg 192  
 Ala Val Ile Trp Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Glu Ser Val  
 50 55 60

aag ggc cga ttc atc atc tcc aga gac aat tcc aag aac acc ctg tat 240  
 Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtc tat tac tgt 288  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

gcg aga gat cgg ggg tcg gta gag atg gct aca atc gcg gac tac tgg 336  
 Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp  
 100 105 110

ggc cag gga acc ctg gtc acc gtc tcc tca 366  
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 115 120

<210> 24

<211> 122

<212> PRT

<213> Homo sapiens

<400> 24

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr  
 20 25 30

2 6 / 1 4 1

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ala Val Ile Trp Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Asp Arg Gly Ser Val Glu Met Ala Thr Ile Ala Asp Tyr Trp

100

105

110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 25

<211> 370

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (369)

<223>

<400> 25

cag gta cag ctg cag cag tca ggt cca gga ctg gtg aag ccc tcg cag

48

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1

5

10

15

acc ctc tca ctc acc tgt gcc atc tcc ggg gac agt gtc tct agc aac

96

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn

27/141

20

25

30

agt gct gct tgg cac tgg atc agg cag tcc cca tcg aga ggc ctt gag 144  
 Ser Ala Ala Trp His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu  
 35 40 45

tgg ctg gga agg aca tac tac agg tcc aag tgg tat aat gat tat aca 192  
 Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Thr  
 50 55 60

gtg tct gtg aaa agt cga ata acc atc aag cca gac aca tcc aag aac 240  
 Val Ser Val Lys Ser Arg Ile Thr Ile Lys Pro Asp Thr Ser Lys Asn  
 65 70 75 80

cag ttc tcc ctg cag ctg aac tct gtg act ccc gag gac acg gct gtg 288  
 Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val  
 85 90 95

tat tac tgt gca aga tca cag gaa gag cac cgg tcg ttg gat gat gct 336  
 Tyr Tyr Cys Ala Arg Ser Gln Glu Glu His Arg Ser Leu Asp Asp Ala  
 100 105 110

ttt gat atc tgg gac cac ggt cac cgt ctc ctc a 370  
 Phe Asp Ile Trp Asp His Gly His Arg Leu Leu  
 115 120

<210> 26

<211> 123

<212> PRT

<213> Homo sapiens

<400> 26

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
 1 5 10 15

2 8 / 1 4 1

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn  
20 25 30

Ser Ala Ala Trp His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu  
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Thr  
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Lys Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Ser Gln Glu Glu His Arg Ser Leu Asp Asp Ala  
100 105 110

Phe Asp Ile Trp Asp His Gly His Arg Leu Leu  
115 120

<210> 27

<211> 360

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (360)

<223>

<400> 27

cag gtc cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc  
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15

29 / 141

tca	gtg	aag	gtc	tcc	tgt	cag	gct	tct	gga	tac	atg	ttc	acc	ggc	ttc	96
Ser	Val	Lys	Val	Ser	Cys	Gln	Ala	Ser	Gly	Tyr	Met	Phe	Thr	Gly	Phe	
			20					25					30			

tat	atg	cac	tgg	gtg	cga	cag	gcc	cct	gga	caa	ggg	ctt	gag	tgg	atg	144
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
		35					40					45				

gga	tgg	atg	aac	act	aac	agt	ggg	gcc	aca	ggc	tat	gca	cac	aag	ttt	192
Gly	Trp	Met	Asn	Thr	Asn	Ser	Gly	Ala	Thr	Gly	Tyr	Ala	His	Lys	Phe	
	50					55					60					

cag	gac	agg	gtc	acc	ctg	acc	agg	gac	acg	tcc	atc	agc	aca	ggc	tac	240
Gln	Asp	Arg	Val	Thr	Leu	Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Gly	Tyr	
65					70					75				80		

atg	gag	ctg	ggc	ggc	ctg	aca	tct	gac	gac	acg	gcc	gtg	tat	tat	tgt	288
Met	Glu	Leu	Gly	Gly	Leu	Thr	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90					95			

gcg	aga	acc	cag	gag	gtt	tac	tac	tac	gct	atg	gac	gtc	tgg	ggc	caa	336
Ala	Arg	Thr	Gln	Glu	Val	Tyr	Tyr	Tyr	Ala	Met	Asp	Val	Trp	Gly	Gln	
			100					105					110			

ggg	aca	atg	gtc	acc	gtc	tct	tca									360
Gly	Thr	Met	Val	Thr	Val	Ser	Ser									
		115				120										

<210> 28

<211> 120

<212> PRT

<213> Homo sapiens

<400> 28

3 0 / 1 4 1

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1                      5                      10                      15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe  
                    20                      25                      30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
                    35                      40                      45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe  
                    50                      55                      60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr  
65                      70                      75                      80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
                    85                      90                      95

Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln  
                    100                      105                      110

Gly Thr Met Val Thr Val Ser Ser  
                    115                      120

<210> 29

<211> 348

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (348)

<223>

<400> 29

3 1 / 1 4 1

cag gtc cag ctg gtg caa tct ggg gct gag gtg agg aag ccc ggg acg 48  
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Thr  
1 5 10 15

aca gtg aca atc tcc tgc aag gtt tct gga cac aac ttc atc gac cac 96  
Thr Val Thr Ile Ser Cys Lys Val Ser Gly His Asn Phe Ile Asp His  
20 25 30

tac atg cat tgg gta caa cag gcc cct gga aaa ggg ctt gac tgg atg 144  
Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Asp Trp Met  
35 40 45

gga cta att gac cct gaa gat ggt cag acg aaa tat tca gag agg ttt 192  
Gly Leu Ile Asp Pro Glu Asp Gly Gln Thr Lys Tyr Ser Glu Arg Phe  
50 55 60

gag ggc aga gtc aca att acc gcg gac aag tca aca gac aca acc tac 240  
Glu Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asp Thr Thr Tyr  
65 70 75 80

ttg gag gtg agc ggc ctg aga tcg gaa gac acg gcc gtt tat ttc tgt 288  
Leu Glu Val Ser Gly Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys  
85 90 95

aca acg gac ttg ggt gac ttg aat tat tgg ggc cag gga acc ctg gtc 336  
Thr Thr Asp Leu Gly Asp Leu Asn Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

acc gtc tcc tca 348  
Thr Val Ser Ser  
115

<210> 30

<211> 116

<212> PRT

3 2 / 1 4 1

<213> Homo sapiens

<400> 30

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Thr  
1 5 10 15

Thr Val Thr Ile Ser Cys Lys Val Ser Gly His Asn Phe Ile Asp His  
20 25 30

Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Asp Trp Met  
35 40 45

Gly Leu Ile Asp Pro Glu Asp Gly Gln Thr Lys Tyr Ser Glu Arg Phe  
50 55 60

Glu Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asp Thr Thr Tyr  
65 70 75 80

Leu Glu Val Ser Gly Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys  
85 90 95

Thr Thr Asp Leu Gly Asp Leu Asn Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser  
115

<210> 31

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(366)



&lt;223&gt;

&lt;400&gt; 31

cag gtc cag ctg gtg caa tct ggg gga ggc gtg gtc cag cct ggg agg 48  
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc aat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn  
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144  
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

gca gtt ata tgg tat gat gga agt aat aaa tac tat gca gac tcc gtg 192  
 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac aca ctg tat 240  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

gcg aga gat cac ggc ctt ggt gat caa gcc tcc tgg ttc gac ccc tgg 336  
 Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp  
 100 105 110

ggc cag ggc acc ctg gtc acc gtc tcc tca 366  
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 115 120

3 4 / 1 4 1

<210> 32

<211> 122

<212> PRT

<213> Homo sapiens

<400> 32

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp  
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 33

<211> 368

<212> DNA

<213> Homo sapiens

3 5 / 1 4 1

<220>

<221> CDS

<222> (1).. (366)

<223>

<400> 33

cag gtc cag ctg gtg caa tct ggg gct gag gtg aag aag tct ggg gcc	48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Ser Gly Ala	
1                      5                      10                      15	

tca gtg aag gtc tcc tgc aag gct tct gga tac acc ttc acc ggc cac	96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly His	
20                      25                      30	

ttt atc cac tgg gtg cgg cag gcc cct gga caa ggg ctt gag tgg atg	144
Phe Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	
35                      40                      45	

gga tgg atc aac cct aac gtt ggt gtc aca aat tat gca cag aag ttt	192
Gly Trp Ile Asn Pro Asn Val Gly Val Thr Asn Tyr Ala Gln Lys Phe	
50                      55                      60	

cag ggc agg gtc acc atg acc agg gac acg tcc ata agc aca gcc tac	240
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr	
65                      70                      75                      80	

ata gaa ctg agg agg ctg aga tct gac gac acg gcc gtg tat tac tgt	288
Ile Glu Leu Arg Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys	
85                      90                      95	

gtg aga gaa tcc gac aca gct gcg gtg gcc tac tac tac cac ggt atg	336
Val Arg Glu Ser Asp Thr Ala Ala Val Ala Tyr Tyr Tyr His Gly Met	
100                      105                      110	

gac gtc tgg gga caa tgg tca ccg tct ctt ca	368
Asp Val Trp Gly Gln Trp Ser Pro Ser Leu	

3 6 / 1 4 1

115

120

<210> 34

<211> 122

<212> PRT

<213> Homo sapiens

<400> 34

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Ser Gly Ala  
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly His  
20 25 30

Phe Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

Gly Trp Ile Asn Pro Asn Val Gly Val Thr Asn Tyr Ala Gln Lys Phe  
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Ile Glu Leu Arg Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Val Arg Glu Ser Asp Thr Ala Ala Val Ala Tyr Tyr Tyr His Gly Met  
100 105 110

Asp Val Trp Gly Gln Trp Ser Pro Ser Leu  
115 120

<210> 35

<211> 375

37 / 141

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(375)

<223>

<400> 35

cag gtc cag ctg gtg caa tct ggg gga gac tgg gta aag cct ggg ggg 48  
Gln Val Gln Leu Val Gln Ser Gly Gly Asp Trp Val Lys Pro Gly Gly  
1 5 10 15

tcc ctt aga ctc tcc tgt gca gcg tct gga ttc cct ttc gct aat gcc 96  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ala Asn Ala  
20 25 30

tgg atg tat tgg ttc cgc cag gct cca ggg aag ggg ctg gag tgg gtt 144  
Trp Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

ggc cgt att aaa agc aaa cca agt ggt ggg gct aca gag ttc gct gca 192  
Gly Arg Ile Lys Ser Lys Pro Ser Gly Gly Ala Thr Glu Phe Ala Ala  
50 55 60

ccc gtg gaa ggt aga ttc agc atc tcc aga gac gat tcg aaa aac acg 240  
Pro Val Glu Gly Arg Phe Ser Ile Ser Arg Asp Asp Ser Lys Asn Thr  
65 70 75 80

atg gat ctg caa atg aat agc ctg aga acc gac gac aca gcc gta tat 288  
Met Asp Leu Gln Met Asn Ser Leu Arg Thr Asp Asp Thr Ala Val Tyr  
85 90 95

tat tgt acc aca gat tgg ggt tcg ggg acc tat cat aag ttt gct tta 336  
Tyr Cys Thr Thr Asp Trp Gly Ser Gly Thr Tyr His Lys Phe Ala Leu  
100 105 110

3 8 / 1 4 1

gat gtc tgg ggc caa ggg aca atg gtc acc gtc tct tca

375

Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser

115

120

125

<210> 36

<211> 125

<212> PRT

<213> Homo sapiens

<400> 36

Gln Val Gln Leu Val Gln Ser Gly Gly Asp Trp Val Lys Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ala Asn Ala

20

25

30

Trp Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Gly Arg Ile Lys Ser Lys Pro Ser Gly Gly Ala Thr Glu Phe Ala Ala

50

55

60

Pro Val Glu Gly Arg Phe Ser Ile Ser Arg Asp Asp Ser Lys Asn Thr

65

70

75

80

Met Asp Leu Gln Met Asn Ser Leu Arg Thr Asp Asp Thr Ala Val Tyr

85

90

95

Tyr Cys Thr Thr Asp Trp Gly Ser Gly Thr Tyr His Lys Phe Ala Leu

100

105

110

Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser

115

120

125

<210> 37  
 <211> 357  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(357)  
 <223>

<400> 37

gtg cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc tca 48  
 Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser  
 1 5 10 15

gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc tat 96  
 Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr  
 20 25 30

atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg gga 144  
 Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly  
 35 40 45

tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt cag 192  
 Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln  
 50 55 60

gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac atg 240  
 Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met  
 65 70 75 80

gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt gcg 288  
 Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

40/141

aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa ggg 336  
Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln Gly  
100 105 110

aca atg gtc acc gtc tct tca 357  
Thr Met Val Thr Val Ser Ser  
115

<210> 38

<211> 119

<212> PRT

<213> Homo sapiens

<400> 38

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser  
1 5 10 15

Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr  
20 25 30

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly  
35 40 45

Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln  
50 55 60

Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met  
65 70 75 80

Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln Gly  
100 105 110



4 1 / 1 4 1

Thr Met Val Thr Val Ser Ser

115

<210> 39

<211> 360

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(360)

<223>

<400> 39

cag	gtg	cag	ctg	gtg	caa	tct	ggg	gct	gag	gtg	aag	aag	cct	ggg	gcc	48
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	
1			5					10						15		

tca	gtg	aag	gtc	tcc	tgt	cag	gct	tct	gga	tac	atg	ttc	acc	ggc	ttc	96
Ser	Val	Lys	Val	Ser	Cys	Gln	Ala	Ser	Gly	Tyr	Met	Phe	Thr	Gly	Phe	
			20					25						30		

tat	atg	cac	tgg	gtg	cga	cag	gcc	cct	gga	caa	ggg	ctt	gag	tgg	atg	144
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
			35					40						45		

gga	tgg	atg	aac	act	aac	agt	ggt	gcc	aca	ggc	tat	gca	cac	aag	ttt	192
Gly	Trp	Met	Asn	Thr	Asn	Ser	Gly	Ala	Thr	Gly	Tyr	Ala	His	Lys	Phe	
			50					55						60		

cag	gac	agg	gtc	acc	ctg	acc	agg	gac	acg	tcc	atc	agc	aca	ggc	tac	240
Gln	Asp	Arg	Val	Thr	Leu	Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Gly	Tyr	
			65					70						75		80

atg	gag	ctg	ggc	ggc	ctg	aca	tct	gac	gac	acg	gcc	gtg	tat	tat	tgt	288
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 2 / 1 4 1

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

gcg aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa 336  
Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln  
100 105 110

ggg aca atg gtc acc gtc tct tca 360  
Gly Thr Met Val Thr Val Ser Ser  
115 120

<210> 40

<211> 120

<212> PRT

<213> Homo sapiens

<400> 40

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe  
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe  
50 55 60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr  
65 70 75 80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

4 3 / 1 4 1

Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln  
100 105 110

Gly Thr Met Val Thr Val Ser Ser  
115 120

<210> 41  
<211> 360  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1).. (360)  
<223>

<400> 41  
cag gtc cag ctg gtg caa tct ggg gct gag gcg aag aag cct ggg gcc 48  
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Ala Lys Lys Pro Gly Ala  
1 5 10 15

tca gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc 96  
Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe  
20 25 30

tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144  
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

gga tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt 192  
Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe  
50 55 60

cag gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac 240  
Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr

4 4 / 1 4 1

65		70		75		80	
atg gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt							288
Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys							
		85		90		95	

gcg aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa							336
Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln							
		100		105		110	

ggg acc acg gtc acc gtc tcc tca							360
Gly Thr Thr Val Thr Val Ser Ser							
		115		120			

<210> 42  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 42						
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Ala Lys Lys Pro Gly Ala						
1		5		10		15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe						
		20		25		30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met						
		35		40		45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe						
		50		55		60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr						
65		70		75		80

4 5 / 1 4 1

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln  
100 105 110

Gly Thr Thr Val Thr Val Ser Ser  
115 120

<210> 43

<211> 369

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (369)

<223>

<400> 43

cag gtc cag ctg gtg caa tct ggg gga ggc ttg gta cag cca ggg cgg 48  
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

tcc ctg aga ctc tcc tgt aca act tct gga ttc acc ttt agt gat tat 96  
Ser Leu Arg Leu Ser Cys Thr Thr Ser Gly Phe Thr Phe Ser Asp Tyr  
20 25 30

gct ttg agc tgg gtc cgc cag gct cca ggg agg ggg ctg gag tgg gta 144  
Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val  
35 40 45

ggt ttc att aga aat aaa att tat ggt ggg aca aca gat tac gcc gca 192  
Gly Phe Ile Arg Asn Lys Ile Tyr Gly Gly Thr Thr Asp Tyr Ala Ala  
50 55 60

46 / 141

tct gtg aaa ggc aga ttc acc atc tca aga gat gat tcc aaa agt atc 240  
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile  
 65 70 75 80

gcc tat ctg caa atg aac agc ctg aaa acc gag gac tca gcc gtc tat 288  
 Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Ser Ala Val Tyr  
 85 90 95

tac tgt act aga gat tcg ggt gtg gtg act gct gcc tac ttt gac tac 336  
 Tyr Cys Thr Arg Asp Ser Gly Val Val Thr Ala Ala Tyr Phe Asp Tyr  
 100 105 110

tgg ggc cag ggc acc ctg gtc acc gtc tcc tca 369  
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 115 120

<210> 44  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 44  
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Thr Ser Gly Phe Thr Phe Ser Asp Tyr  
 20 25 30

Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val  
 35 40 45

Gly Phe Ile Arg Asn Lys Ile Tyr Gly Gly Thr Thr Asp Tyr Ala Ala  
 50 55 60

47/141

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile  
65 70 75 80

Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Ser Ala Val Tyr  
85 90 95

Tyr Cys Thr Arg Asp Ser Gly Val Val Thr Ala Ala Tyr Phe Asp Tyr  
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 45

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(366)

<223>

<400> 45

cag gtc cag ctg gtg caa tct ggg gga ggc gtg gtc cag cct ggg agg 48  
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc aat 96  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn  
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

48 / 141

gca gtt ata tgg tat gat gga agt aat aaa tac tat gca gac tcc gtg 192  
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac aca ctg tat 240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

gcg aga gat cac ggc ctt ggt gat caa gcc tcc tgg ttc gac ccc tgg 336  
Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp  
100 105 110

ggc cag ggg acc acg gtc acc gtc tcc tca 366  
Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120

<210> 46

<211> 122

<212> PRT

<213> Homo sapiens

<400> 46

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45



4 9 / 1 4 1

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp His Gly Leu Gly Asp Gln Ala Ser Trp Phe Asp Pro Trp  
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120

<210> 47

<211> 360

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(360)

<223>

<400> 47

cag gtc cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc 48  
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15

tca gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc 96  
Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe  
20 25 30

tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144

50/141

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

gga tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt 192  
Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe  
50 55 60

cag gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac 240  
Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr  
65 70 75 80

atg gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt 288  
Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

gcg aga acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa 336  
Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln  
100 105 110

ggg aca atg gtc acc gtc tct tca 360  
Gly Thr Met Val Thr Val Ser Ser  
115 120

<210> 48

<211> 120

<212> PRT

<213> Homo sapiens

<400> 48

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe  
20 25 30

5 1 / 1 4 1

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe  
50 55 60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr  
65 70 75 80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln  
100 105 110

Gly Thr Met Val Thr Val Ser Ser  
115 120

<210> 49  
<211> 353  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1).. (351)  
<223>

<400> 49

cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc tca gtg 48  
Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val  
1 5 10 15

aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc tat atg 96  
Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr Met

5 2 / 1 4 1

20	25	30	
cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg gga tgg His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp			144
35	40	45	
atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt cag gac Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln Asp			192
50	55	60	
agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac atg gag Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met Glu			240
65	70	75	80
ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt gcg aga Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg			288
85	90	95	
acc cag gag gtt tac tac tac gct atg gac gtc tgg ggc caa ggg aca Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln Gly Thr			336
100	105	110	
atg gtc acc gtc tct tc Met Val Thr Val Ser			353
115			

<210> 50

<211> 117

<212> PRT

<213> Homo sapiens

<400> 50

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val

1

5

10

15

5 3 / 1 4 1

Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr Met  
20 25 30

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp  
35 40 45

Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln Asp  
50 55 60

Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met Glu  
65 70 75 80

Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg  
85 90 95

Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln Gly Thr  
100 105 110

Met Val Thr Val Ser  
115

<210> 51

<211> 360

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (360)

<223>

<400> 51

cag gtc cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc  
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15

5 4 / 1 4 1

tca	gtg	aag	gtc	tcc	tgt	cag	gct	tct	gga	tac	atg	ttc	acc	ggc	ttc	96
Ser	Val	Lys	Val	Ser	Cys	Gln	Ala	Ser	Gly	Tyr	Met	Phe	Thr	Gly	Phe	
			20					25						30		

tat	atg	cac	tgg	gtg	cga	cag	gcc	cct	gga	caa	ggg	ctt	gag	tgg	atg	144
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
		35					40					45				

gga	tgg	atg	aac	act	aac	agt	ggt	gcc	aca	ggc	tat	gca	cac	aag	ttt	192
Gly	Trp	Met	Asn	Thr	Asn	Ser	Gly	Ala	Thr	Gly	Tyr	Ala	His	Lys	Phe	
	50					55					60					

cag	gac	agg	gtc	acc	ctg	acc	agg	gac	acg	tcc	atc	agc	aca	ggc	tac	240
Gln	Asp	Arg	Val	Thr	Leu	Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Gly	Tyr	
65					70					75				80		

atg	gag	ctg	ggc	ggc	ctg	aca	tct	gac	gac	acg	gcc	gtg	tat	tat	tgt	288
Met	Glu	Leu	Gly	Gly	Leu	Thr	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90					95			

gcg	aga	acc	cag	gag	gtt	tac	tac	tac	gct	atg	gac	gtc	tgg	ggc	caa	336
Ala	Arg	Thr	Gln	Glu	Val	Tyr	Tyr	Tyr	Ala	Met	Asp	Val	Trp	Gly	Gln	
			100					105					110			

gga	acc	ctg	gtc	acc	gtc	tct	tca									360
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser									
		115				120										

<210> 52

<211> 120

<212> PRT

<213> Homo sapiens

<400> 52

5 5 / 1 4 1

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe

20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35 40 45

Gly Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe

50 55 60

Gln Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr

65 70 75 80

Met Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 53

<211> 357

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (357)

<223>

<400> 53

56 / 141

gtc cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc tca 48  
Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser  
1 5 10 15

gtg aag gtc tcc tgt cag gct tct gga tac atg ttc acc ggc ttc tat 96  
Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr  
20 25 30

atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg gga 144  
Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly  
35 40 45

tgg atg aac act aac agt ggt gcc aca ggc tat gca cac aag ttt cag 192  
Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln  
50 55 60

gac agg gtc acc ctg acc agg gac acg tcc atc agc aca ggc tac atg 240  
Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met  
65 70 75 80

gag ctg ggc ggc ctg aca tct gac gac acg gcc gtg tat tat tgt gcg 288  
Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

aga acc cag gag gtt tac tac tac gct atg gac gta ctg ggg cca agg 336  
Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Leu Gly Pro Arg  
100 105 110

gac aat ggt cac cgt ctc ttc 357  
Asp Asn Gly His Arg Leu Phe  
115

<210> 54  
<211> 119  
<212> PRT



5 7 / 1 4 1

<213> Homo sapiens

<400> 54

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser  
1                    5                    10                    15

Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Met Phe Thr Gly Phe Tyr  
                  20                    25                    30

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly  
          35                    40                    45

Trp Met Asn Thr Asn Ser Gly Ala Thr Gly Tyr Ala His Lys Phe Gln  
          50                    55                    60

Asp Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Gly Tyr Met  
65                    70                    75                    80

Glu Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala  
                  85                    90                    95

Arg Thr Gln Glu Val Tyr Tyr Tyr Ala Met Asp Val Leu Gly Pro Arg  
          100                    105                    110

Asp Asn Gly His Arg Leu Phe  
          115

<210> 55

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (342)

58/141

<223>

<400> 55

gat att gtg atg acc cag act cca gac tcc ctg gct gtg tct ctg ggc	48
Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly	
1                      5                      10                      15	

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc	96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
20                      25                      30	

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag	144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
35                      40                      45	

cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc	192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	
50                      55                      60	

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc	240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
65                      70                      75                      80	

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa	288
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	
85                      90                      95	

tat tat agt act cct ccg acg ttc ggc caa ggg acc aag gtg gaa atc	336
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	
100                      105                      110	

aaa cgt	342
Lys Arg	

59/141

<210> 56  
<211> 114  
<212> PRT  
<213> Homo sapiens

<400> 56

Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly  
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg

<210> 57  
<211> 337  
<212> DNA  
<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1).. (336)

&lt;223&gt;

&lt;400&gt; 57

gat	ctt	gtg	atg	act	cag	tct	cca	gac	tcc	ctg	gct	gtg	tct	ctg	ggc	48
Asp	Leu	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly	
1				5					10					15		

gag	agg	gcc	acc	atc	aac	tgc	aag	tcc	agc	cag	agt	gtt	tta	tac	agc	96
Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser	
			20					25					30			

tcc	aac	aat	aag	aac	tac	tta	gct	tgg	cac	cag	cag	aaa	cca	gga	cag	144
Ser	Asn	Asn	Lys	Asn	Tyr	Leu	Ala	Trp	His	Gln	Gln	Lys	Pro	Gly	Gln	
			35				40					45				

cct	cct	aaa	ctg	ctc	att	tac	tgg	gca	tct	acc	cgg	gaa	tcc	ggg	gtc	192
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val	
		50				55				60						

cct	gac	cga	ttc	agt	ggc	agc	ggg	tct	ggg	aca	gat	ttc	act	ctc	acc	240
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	
65					70				75					80		

atc	agc	acc	ctg	cag	gct	gaa	gat	gtg	gca	gtt	tat	tac	tgt	cag	caa	288
Ile	Ser	Thr	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	
			85					90						95		

tat	tat	agt	act	cct	ccg	acg	ttc	ggc	caa	ggg	acc	aaa	gtg	gat	atc	a	337
Tyr	Tyr	Ser	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Asp	Ile		
			100					105					110				

&lt;210&gt; 58

6 1 / 1 4 1

<211> 112

<212> PRT

<213> Homo sapiens

<400> 58

Asp Leu Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
1                    5                    10                    15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
                  20                    25                    30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp His Gln Gln Lys Pro Gly Gln  
                  35                    40                    45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
                  50                    55                    60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65                    70                    75                    80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
                  85                    90                    95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Asp Ile  
                  100                    105                    110

<210> 59

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (342)

<223>

6 2 / 1 4 1

<400> 59

gat att gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc	48
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
1                      5                      10                      15	

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc	96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
20                      25                      30	

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag	144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
35                      40                      45	

cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc	192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	
50                      55                      60	

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc	240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
65                      70                      75                      80	

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa	288
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	
85                      90                      95	

tat tat agt act cct ccg acg ttc ggc caa ggg acc aag gtg gaa atc	336
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	
100                      105                      110	

aaa cgt	342
Lys Arg	

<210> 60

6 3 / 1 4 1

<211> 114

<212> PRT

<213> Homo sapiens

<400> 60

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
1                      5                      10                      15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
                    20                      25                      30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
                    35                      40                      45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
                    50                      55                      60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65                      70                      75                      80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
                    85                      90                      95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
                    100                      105                      110

Lys Arg

<210> 61

<211> 342

<212> DNA

<213> Homo sapiens

<220>

6 4 / 1 4 1

<221> CDS

<222> (1).. (342)

<223>

<400> 61

gat att gtg atg act cag tct cca ctc tcc ctg ccc gtc acc cct gga	48
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly	
1                      5                      10                      15	

gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ttg gat agt	96
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser	
20                      25                      30	

gat gat gga aac acc tat ttg gac tgg tac ctg cag aag cca ggg cag	144
Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln	
35                      40                      45	

tct cca cag ctc cta atc tat acg ctt tcc tat cgg gcc tct gga gtc	192
Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val	
50                      55                      60	

cca gac agg ttc agt ggc agt ggg tca ggc act gat ttc aca ctg aaa	240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys	
65                      70                      75                      80	

atc agc agg gtg gag gct gag gat gtt gga gtt tat tac tgc atg caa	288
Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln	
85                      90                      95	

cgt ata gag ttt cct tac act ttt ggc cag ggg acc aaa gtg gat atc	336
Arg Ile Glu Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Asp Ile	
100                      105                      110	

aaa cgt	342
Lys Arg	



6 5 / 1 4 1

<210> 62

<211> 114

<212> PRT

<213> Homo sapiens

<400> 62

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly  
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser  
20 25 30

Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln  
35 40 45

Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val  
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys  
65 70 75 80

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln  
85 90 95

Arg Ile Glu Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Asp Ile  
100 105 110

Lys Arg

<210> 63

<211> 342

<212> DNA

6 6 / 1 4 1

<213> Homo sapiens

$\langle 220 \rangle$

&lt;221&gt; CDS

**<222> (1).. (342)**

<223>

<400> 63

gat gtt gtg atg act cag tct cca ctc tcc ctg ccc gtc acc cct gga 48  
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly  
1 5 10 15

gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ttg gat agt 96  
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser  
20 25 30

gat gat gga aac acc tat ttg gac tgg tac ctg cag aag cca ggg cag 144  
Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln  
35 40 45

tct cca cag ctc cta atc tat acg ctt tcc tat cgg gcc tct gga gtc 192  
Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val  
50 55 60

cca gac agg ttc agt ggc agt ggg tca ggc act gat ttc aca ctg aaa 240  
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys  
65 70 75 80

atc agc agg gtg gag gct gag gat gtt gga gtt tat tac tgc atg caa 288  
Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln  
85 90 95

cgt ata gag ttt cct tac act ttt ggc cag ggg acc aag gtg gaa atc 336  
Arg Ile Glu Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
100 105 110

67/141

aaa cgt

342

Lys Arg

<210> 64

<211> 114

<212> PRT

<213> Homo sapiens

<400> 64

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly  
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser  
20 25 30

Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln  
35 40 45

Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val  
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys  
65 70 75 80

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln  
85 90 95

Arg Ile Glu Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg

6 8 / 1 4 1

<210> 65  
<211> 339  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(339)  
<223>

<400> 65  
gat att gtg atg acc cag act cca ctc tcc ctg ccc gtc acc cct gga 48  
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly  
1 5 10 15

gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ttg gat agt 96  
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser  
20 25 30

gat gat gga aac acc tat ttg gac tgg tac ctg cag aag cca ggg cag 144  
Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln  
35 40 45

tct cca cag ctc cta atc tat acg ctt tcc tat cgg gcc tct gga gtc 192  
Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val  
50 55 60

cca gac agg ttc agt ggc agt ggg tca ggc act gat ttc aca ctg aaa 240  
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys  
65 70 75 80

atc agc agg gtg gag gct gag gat gtt gga gtt tat tac tgc atg caa 288  
Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln  
85 90 95

gct aca caa ttg tac act ttt ggc cag ggg acc aag gtg gag atc aaa 336

6 9 / 1 4 1

Ala Thr Gln Leu Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105 110

cgt

339

Arg

<210> 66

<211> 113

<212> PRT

<213> Homo sapiens

<400> 66

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly  
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser  
20 25 30

Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln  
35 40 45

Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val  
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys  
65 70 75 80

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln  
85 90 95

Ala Thr Gln Leu Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105 110

Arg

70/141

<210> 67  
<211> 342  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(342)  
<223>

<400> 67

gat att gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc 48  
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96  
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144  
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192  
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240  
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288  
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln

7 1 / 1 4 1

85

90

95

tat tat agt act cct ccg acg ttc ggc caa ggg acc aag ctg gag atc 336  
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile  
100 105 110

aaa cgt 342  
Lys Arg

<210> 68

<211> 114

<212> PRT

<213> Homo sapiens

<400> 68

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile

7 2 / 1 4 1

100

105

110

Lys Arg

<210> 69

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (342)

<223>

<400> 69

gat gtt gtg atg act cag act cca gac tcc ctg gct gtg tct ctg ggc 48

Asp Val Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly

1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta cac aag 96

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu His Lys

20 25 30

tcc aac aat aag aac tat tta gct tgg tac cag cag aaa cca gga cag 144

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln

35 40 45

cct cct aaa ttg ctc att cac tgg gct tct acc cgg gaa ttc ggg gtc 192

Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val

50 55 60

cct gac cga ctc agt ggc agc ggg tct gcg aca gat ttc act ctc acc 240

Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr

65 70 75 80



7 3 / 1 4 1

atc agc agc ctg cag gct gaa gac gtg gca gtc tat tac tgt cag caa 288  
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

tat tat gct gtt cct ctc acc ttc ggc caa ggg aca cga ctg gag att 336  
Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile  
100 105 110

aaa cgt 342  
Lys Arg

<210> 70  
<211> 114  
<212> PRT  
<213> Homo sapiens

<400> 70  
Asp Val Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly  
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu His Lys  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val  
50 55 60

Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln

7 4 / 1 4 1

85

90

95

Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile  
100 105 110

Lys Arg

<210> 71

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (342)

<223>

<400> 71

gat att gtg atg acc cag acg cca gac tcc ctg gct gtg tct ctg ggc 48  
Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly  
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96  
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144  
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192  
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

7 5 / 1 4 1

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240  
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288  
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

tat tat agt act cct ccg acg ttc agc caa ggg acc aag gtg gaa atc 336  
Tyr Tyr Ser Thr Pro Pro Thr Phe Ser Gln Gly Thr Lys Val Glu Ile  
100 105 110

aaa cgt 342  
Lys Arg

<210> 72  
<211> 114  
<212> PRT  
<213> Homo sapiens

<400> 72  
Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly  
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

7 6 / 1 4 1

65		70		75		80									
Ile	Ser	Thr	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln
			85					90					95		
Tyr	Tyr	Ser	Thr	Pro	Pro	Thr	Phe	Ser	Gln	Gly	Thr	Lys	Val	Glu	Ile
			100					105					110		
Lys	Arg														

<210> 73  
 <211> 342  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(342)  
 <223>

<400> 73

gat	gtt	gtg	atg	act	cag	tct	cca	gac	tcc	ctg	act	gtg	tct	ctg	ggc	48
Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Thr	Val	Ser	Leu	Gly	
1			5					10					15			
gag	agg	gcc	acc	atc	aac	tgc	aag	tcc	agc	cag	agt	gtt	tta	tac	agc	96
Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser	
			20				25					30				
tcc	aac	aat	aag	aac	tac	tta	gct	tgg	tac	cag	cag	aaa	cca	gga	cag	144
Ser	Asn	Asn	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	
			35				40					45				
cct	cct	aag	ctg	ctc	att	tac	tgg	gca	cct	acc	cgg	gaa	tcc	ggg	gtc	192

7 7 / 1 4 1

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Pro Thr Arg Glu Ser Gly Val  
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240  
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288  
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

tat tat agt act cct ccg acg ttc ggc cag ggg acc aag gtg gaa atc 336  
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
100 105 110

aaa cgt 342  
Lys Arg

<210> 74

<211> 114

<212> PRT

<213> Homo sapiens

<400> 74

Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Thr Val Ser Leu Gly  
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Pro Thr Arg Glu Ser Gly Val

7 8 / 1 4 1

50		55		60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr				
65		70		75
				80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln				
	85		90	95
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile				
	100		105	110

Lys Arg

<210> 75  
 <211> 342  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(342)  
 <223>

<400> 75	
gat gtt gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc	48
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
1                      5                      10                      15	
gag agg gcc acc atc aac tgc aag tcc agc cag ggt gtt tta cac aag	96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Gly Val Leu His Lys	
20                      25                      30	
tcc aac aat aag aac tat tta gct tgg tac cag cag aaa cca gga cag	144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	

7 9 / 1 4 1

35

40

45

cct cct aaa ttg ctc att cac tgg gct tct acc cgg gaa ttc ggg gtc 192  
Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val  
50 55 60

cct gac cga ctc agt ggc agc ggg tct gcg aca gat ttc act ctc acc 240  
Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr  
65 70 75 80

atc agc agc ctg cag gct gaa gac gtg gca gtc tat tac tgt cag caa 288  
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

tat tat gct gtt cct ctc acc ttc ggc caa ggg aca cga ctg gag att 336  
Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile  
100 105 110

aaa cgt 342  
Lys Arg

<210> 76

<211> 114

<212> PRT

<213> Homo sapiens

<400> 76

Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Gly Val Leu His Lys  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln

80 / 141

35

40

45

Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val  
50 55 60

Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile  
100 105 110

Lys Arg

<210> 77

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (342)

<223>

<400> 77

gat att gtg atg acc cag acg cca gac tcc ctg gct gtg tct ctg ggc 48  
Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly  
1 5 10 15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96  
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30



81 / 141

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144  
 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
 35 40 45

cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192  
 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240  
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288  
 Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
 85 90 95

tat tat agt act cct ccg acg ttc ggc caa ggg acc aag gtg gaa atc 336  
 Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
 100 105 110

aaa cgt 342  
 Lys Arg

<210> 78

<211> 114

<212> PRT

<213> Homo sapiens

<400> 78

Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly  
 1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser

8 2 / 1 4 1

20

25

30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg

<210> 79

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (342)

<223>

<400> 79

gat gtt gtg atg act cag tct cca gac tcc ctg gct gtg cct ctg ggc  
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Pro Leu Gly  
1 5 10 15

48

83/141

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta cac aag 96  
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu His Lys  
 20 25 30

tcc aac aat aag aac cat tta gct tgg tac cag cag aaa cca gga cag 144  
 Ser Asn Asn Lys Asn His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
 35 40 45

cct cct aaa ttg ctc att cac tgg gct tct acc cgg gaa ttc ggg gtc 192  
 Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val  
 50 55 60

cct gac cga ctc agt ggc agc ggg tct gcg aca gat ttc act ctc acc 240  
 Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr  
 65 70 75 80

atc aac agc ctg cag gct gaa gac gcg gca gtc tat tac tgt cag caa 288  
 Ile Asn Ser Leu Gln Ala Glu Asp Ala Ala Val Tyr Tyr Cys Gln Gln  
 85 90 95

tat tat gct gtt cct ctc acc ttc ggc caa ggg aca cga ctg gag att 336  
 Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile  
 100 105 110

aaa cgt 342  
 Lys Arg

<210> 80

<211> 114

<212> PRT

<213> Homo sapiens

<400> 80

Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Pro Leu Gly

8 4 / 1 4 1

1	5	10	15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu His Lys			
20	25	30	
Ser Asn Asn Lys Asn His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln			
35	40	45	
Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val			
50	55	60	
Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr			
65	70	75	80
Ile Asn Ser Leu Gln Ala Glu Asp Ala Ala Val Tyr Tyr Cys Gln Gln			
85	90	95	
Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile			
100	105	110	

Lys Arg

<210> 81  
 <211> 342  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1).. (342)  
 <223>

<400> 81

gat att gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc

8 5 / 1 4 1

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
1                5                      10                          15

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96  
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144  
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192  
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240  
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288  
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

tat tat agt act cct ccg acg ttc ggc caa ggg acc aaa gtg gat atc 336  
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Asp Ile  
100 105 110

aaa cgt	342
Lys Arg	

**<210> 82**

<211> 114

&lt;212&gt; PRT

<213> Homo sapiens

86 / 141

<400> 82

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Asp Ile  
100 105 110

Lys Arg

<210> 83

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (342)

<223>

&lt;400&gt; 83

gat gtt gtg atg act cag tct cca gac tcc ctg gct gtg tct ctg ggc	48
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
1                      5                      10                      15	

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc	96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
20                      25                      30	

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag	144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
35                      40                      45	

cct cct aaa ttg ctc att cac tgg gct tct acc cgg gaa ttc ggg gtc	192
Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val	
50                      55                      60	

cct gac cga ctc agt ggc agc ggg tct gcg aca gat ttc act ctc acc	240
Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr	
65                      70                      75                      80	

atc agc agc ctg cag gct gaa gac gtg gca gtc tat tac tgt cag caa	288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	
85                      90                      95	

tat tat gct gtt cct ctc acc ttc ggc caa ggg aca cga ctg gag att	336
Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile	
100                      105                      110	

aaa cgt	342
Lys Arg	

&lt;210&gt; 84

88/141

<211> 114

<212> PRT

<213> Homo sapiens

<400> 84

Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Glu Phe Gly Val  
50 55 60

Pro Asp Arg Leu Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Ala Val Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile  
100 105 110

Lys Arg

<210> 85

<211> 342

<212> DNA

<213> Homo sapiens

<220>



&lt;221&gt; CDS

&lt;222&gt; (1)..(342)

&lt;223&gt;

&lt;400&gt; 85

gac atc gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc	48
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
1                      5                      10                      15	

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc	96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
20                      25                      30	

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag	144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
35                      40                      45	

cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc	192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	
50                      55                      60	

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc	240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
65                      70                      75                      80	

atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa	288
Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	
85                      90                      95	

tat tat agt act cct ccg acg ttc ggc caa ggg acc aag gtg gaa atc	336
Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	
100                      105                      110	

aaa cgt	342
Lys Arg	

90/141

<210> 86

<211> 114

<212> PRT

<213> Homo sapiens

<400> 86

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg

<210> 87

<211> 327

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(327)

<223>

<400> 87

gaa att gtg ctg act cag tct cca ggc acc ctg tct ttg tct cca ggg 48  
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

gaa aga gcc acc ctc tcc tgc aag gcc agt cag agt ttt agc agc aac 96  
Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser Phe Ser Ser Asn  
20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctg ctc 144  
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192  
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

ggc agt aaa tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240  
Gly Ser Lys Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

cct gaa gat ttt gca gtg tat tac tgt cag cag tat gtt acc tca ccg 288  
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Thr Ser Pro  
85 90 95

tac act ttt ggc ctg ggg acc aag gtg gag atc aaa cgt 327  
Tyr Thr Phe Gly Leu Gly Thr Lys Val Glu Ile Lys Arg  
100 105

9 2 / 1 4 1

<210> 88  
<211> 109  
<212> PRT  
<213> Homo sapiens

<400> 88

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
1                    5                    10                    15

Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser Phe Ser Ser Asn  
                  20                    25                    30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
                  35                    40                    45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
                  50                    55                    60

Gly Ser Lys Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65                    70                    75                    80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Thr Ser Pro  
                  85                    90                    95

Tyr Thr Phe Gly Leu Gly Thr Lys Val Glu Ile Lys Arg  
                  100                    105

<210> 89  
<211> 325  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS

9 3 / 1 4 1

<222> (1).. (324)

<223>

<400> 89

gat gtt ggg atg aca cag tct tca gcc acc cta tct ttg tct cca ggg 48  
Asp Val Gly Met Thr Gln Ser Ser Ala Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agg att agc agt tat 96  
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Ile Ser Ser Tyr  
20 25 30

tta gcc tgg tac caa cag aaa cct ggc cag gct ccc aga ctc ctc atc 144  
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
35 40 45

tat gag gca gtc aaa agg gcc act ggc atc cca gcc agg ttc agt ggc 192  
Tyr Glu Ala Val Lys Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
50 55 60

agt ggg tct ggg aca gag ttc acc ctc acc atc aac agc cta gag cct 240  
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Glu Pro  
65 70 75 80

gaa gat ttt gca gtt tat ttc tgt cag cag cgt ggc agc tgt cct ggg 288  
Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Arg Gly Ser Cys Pro Gly  
85 90 95

acg ttc ggc cag ggg acc aag ctg gag atc aaa cgt t 325  
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
100 105

<210> 90

<211> 108

<212> PRT

9 4 / 1 4 1

<213> Homo sapiens

<400> 90

Asp Val Gly Met Thr Gln Ser Ser Ala Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Ile Ser Ser Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
35 40 45

Tyr Glu Ala Val Lys Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Glu Pro  
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Arg Gly Ser Cys Pro Gly  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
100 105

<210> 91

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (366)

<223>

<400> 91

9 5 / 1 4 1

cag gtc cag ctg gtg caa tct ggg gct gag gtg aag aag cct ggg gcc 48  
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15

tca gtg aag gtc tcc tgc aag gct tct gga tac acc ttc acc ggc tac 96  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr  
20 25 30

tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144  
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

gga tgg atc aac cct aac agt ggt ggc aca aag tat gca cag aag ttt 192  
Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala Gln Lys Phe  
50 55 60

cag ggc agg gtc acc atg acc agg gac acg tcc atc agc aca gcc tac 240  
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr  
65 70 75 80

atg gag ctg agc agg ctg aga tct gac gac acg gcc gtg tat tac tgt 288  
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

gcg aga gga tac gat att ttg act ggt tat ggc tgg ttc gac ccc tgg 336  
Ala Arg Gly Tyr Asp Ile Leu Thr Gly Tyr Gly Trp Phe Asp Pro Trp  
100 105 110

ggc cag gga acc ctg gtc acc gtc tcc tca 366  
Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

**<210> 92**

**<211> 122**

&lt;212&gt; PRT

96 / 141

<213> Homo sapiens

<400> 92

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1                      5                      10                      15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr  
                    20                      25                      30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
                    35                      40                      45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala Gln Lys Phe  
                    50                      55                      60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr  
65                      70                      75                      80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
                    85                      90                      95

Ala Arg Gly Tyr Asp Ile Leu Thr Gly Tyr Gly Trp Phe Asp Pro Trp  
                    100                      105                      110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
                    115                      120

<210> 93

<211> 360

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (360)



9 7 / 1 4 1

<223>

<400> 93

cag gtc cag ctg gtg caa tct ggg gga ggc ttg gtc cag cct ggg ggg	48
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
1                      5                      10                      15	

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agt agc tat	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	
20                      25                      30	

tgg atg agt tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtg	144
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35                      40                      45	

gcc aac ata aag caa gat gga agt gag aaa tac tat gtg gac tct gtg	192
Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val	
50                      55                      60	

aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac tca ctg tat	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr	
65                      70                      75                      80	

ctg caa atg aac acc ctg aga gcc gag gac acg gct gtg tat tac tgt	288
Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85                      90                      95	

gcg aga gat cgt ttg tgg acc cag ggg ttt ttt gac tac tgg ggc cag	336
Ala Arg Asp Arg Leu Trp Thr Gln Gly Phe Phe Asp Tyr Trp Gly Gln	
100                      105                      110	

gga acc ctg gtc acc gtc tcc tca	360
Gly Thr Leu Val Thr Val Ser Ser	
115                      120	

98/141

<210> 94  
<211> 120  
<212> PRT  
<213> Homo sapiens

<400> 94

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp Arg Leu Trp Thr Gln Gly Phe Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 95  
<211> 339  
<212> DNA  
<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1).. (339)

&lt;223&gt;

&lt;400&gt; 95

gac atc gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc	48
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
1                      5                      10                      15	

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc	96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
20                      25                      30	

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag	144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
35                      40                      45	

cct cct aac ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc	192
Pro Pro Asn Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	
50                      55                      60	

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc	240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
65                      70                      75                      80	

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa	288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	
85                      90                      95	

tat tat act act ccg tgg acg ttc ggc caa ggg acc aag gtg gaa atc	336
Tyr Tyr Thr Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	
100                      105                      110	

aaa

339

Lys

100/141

<210> 96  
<211> 113  
<212> PRT  
<213> Homo sapiens

<400> 96

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

Pro Pro Asn Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Thr Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
100 105 110

Lys

<210> 97  
<211> 23

1 0 1 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 97

caggtkcagc tggcgcagtc tgg

23

<210> 98

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 98

caggtccagc ttgtgcagtc tgg

23

<210> 99

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 99

saggtccagc tggcgcagtc tgg

23

<210> 100

<211> 23

1 0 2 / 1 4 1

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 100

caratgcagc tggcgcagtc tgg

23

<210> 101

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 101

cagatcacct tgaaggagtc tggt

24

<210> 102

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially Synthesized Primer Sequence

<400> 102

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24

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23

<210> 104

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<400> 104

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23

<210> 105

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<400> 105

gaggtgcagc tggaggagtc tgg

23

<210> 106

<211> 24

1 0 4 / 1 4 1

<212> DNA

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<400> 106

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24

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<400> 107

caggtgcagc tacagcagtg gggc

24

<210> 108

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<400> 108

gargtgcagc tgggtgcagtc tgga

24

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<400> 109

caggtacagc tgcagcagtc aggt

24

<210> 110

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<400> 110

caggtscagc tggcgaatc tgg

23

<210> 111

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tgaggagacg gtgaccaggg tkcc

24

<210> 112

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24

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24

<210> 114

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<400> 114

racatccaga tgacccagtc tcca

24

<210> 115

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24

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24

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gtcatctgga tgacccagtc tcca

24

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1 0 8 / 1 4 1

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24

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24

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24

<210> 121

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1 0 9 / 1 4 1

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24

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24

<210> 123

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gacatcgtga tgacccagtc tcca

24

<210> 124

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1 1 0 / 1 4 1

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24

<210> 125

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<400> 125

gaaattgtgc tgactcagtc tcca

24

<210> 126

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<400> 126

gatgttgtga tgacacagtc tcca

24

<210> 127

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1 1 1 / 1 4 1

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acgtttgatt tccaccttgg tccc

24

<210> 128

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<400> 128

acgtttgatc tccaccttgg tccc

24

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24

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cagtctgtgc tgactcagcc accc

24

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<400> 132

cagtctgtgy tgacgcagcc gccc

24

<210> 133

<211> 22



1 1 3 / 1 4 1

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cagtctgccc tgactcagcc ts

22

<210> 134

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24

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24

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24

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<400> 137

tcctatgagc tgatgcagcc accc

24

<210> 138

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<400> 138

cagcctgtgc tgactcaatc atcc

24

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1 1 5 / 1 4 1

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24

<210> 140

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<400> 140

ctgcctgtgc tgactcagcc cccg

24

<210> 141

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<223> Artificially Synthesized Primer Sequence

<400> 141

cagcctgtgc tgactcagcc ayct

24

<210> 142

<211> 24

1 1 6 / 1 4 1

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24

<210> 143

<211> 24

<212> DNA

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<223> Artificially Synthesized Primer Sequence

<400> 143

aattttatgc tgactcagcc ccac

24

<210> 144

<211> 24

<212> DNA

<213> Artificial

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<223> Artificially Synthesized Primer Sequence

<400> 144

cagrcctgtgg tgactcagga gccc

24

<210> 145

<211> 24

1 1 7 / 1 4 1

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24

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<223> Artificially Synthesized Primer Sequence

<400> 146

cwgccctgtgc tgactcagcc acct

24

<210> 147

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<400> 147

caggcagggc tgactcagcc accc

24

<210> 148

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1 1 8 / 1 4 1

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acctaggacg gtgaccttgg tccc

24

<210> 149

<211> 24

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<400> 149

acctaggacg gtcagcttgg tccc

24

<210> 150

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<400> 150

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24

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<211> 91

1 1 9 / 1 4 1

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gcggatcgga catccagatg acccagtctc c 91

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<400> 152

gcaccctggt caccgtctcc tcaggtgg 28

<210> 153

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<400> 153

ggacaatggt caccgtctct tcaggtgg 28

1 2 0 / 1 4 1

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gaaccctggt cacgtctcc tcaggtgg

28

<210> 155

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<400> 155

ggaccacggt cacgtctcc tcaggtgg

28

<210> 156

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<223> Artificially Synthesized Primer Sequence

<400> 156

ggagactggg tcatctggat gtccgatccg cc

32



1 2 1 / 1 4 1

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32

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ggagactgcg tcaacacaat ttccgatccg cc

32

<210> 159

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ggagactggg tcatacacgat gtccgatccg cc

32

1 2 2 / 1 4 1

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32

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32

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ggcggctgcg tcaacacaga ctgcgatccg ccaccgccag ag

42

1 2 3 / 1 4 1

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<211> 42

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42

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42

<210> 165

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42

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<211> 42

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42

<210> 167

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42

<210> 168

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42

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agtattgacc atggcccagg tgcagctggt gcagtctgg

39

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39

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<400> 172

agtattgacc atggcccagg tgcagctgca ggagtcggg

39

<210> 173

<211> 39

<212> DNA

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<400> 173

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39

<210> 174

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<400> 174

agtattgacc atggcccagg tacagctgca gcagtcagg

39

1 2 7 / 1 4 1

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<400> 175

taatgaattc acgtttgatt tccaccttgg tccc

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<211> 34

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<400> 176

taatgaattc acgtttgatc tccagcttgg tccc

34

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<400> 177

taatgaattc acgtttgata tccactttgg tccc

34

1 2 8 / 1 4 1

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<400> 178

taatgaattc acgtttgatc tccaccttg tccc

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<210> 179

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<400> 179

taatgaattc acgtttaatc tccagtcgtg tccc

34

<210> 180

<211> 34

<212> DNA

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<223> Artificially Synthesized Primer Sequence

<400> 180

taatgaattc acctaggacg gtgaccttg tccc

34



1 2 9 / 1 4 1

<210> 181

<211> 34

<212> DNA

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<400> 181

taatgaattc acctaggacg gtcagcttgg tccc

34

<210> 182

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taatgaattc acctaaaacg gtgagctggg tccc

34

<210> 183

<211> 861

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(861)

<223>

<400> 183

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48

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Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala

1 5 10 15

gcc cag ccg gcg atg gcc atg gcc cag gtg cag ctg gtg cag tct ggg 96

Ala Gln Pro Ala Met Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly

20 25 30

gct gag gtg aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gct 144

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala

35 40 45

tct gga tac acc ttc acc ggc tac tat atg cac tgg gtg cga cag gcc 192

Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala

50 55 60

cct gga caa ggg ctt gag tgg atg gga tgg atc aac cct aac agt ggt 240

Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly

65 70 75 80

ggc aca aag tat gca cag aag ttt cag ggc agg gtc acc atg acc agg 288

Gly Thr Lys Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg

85 90 95

gac acg tcc atc agc aca gcc tac atg gag ctg agc agg ctg aga tct 336

Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser

100 105 110

gac gac acg gcc gtg tat tac tgt gcg aga gga tac gat att ttg act 384

Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Asp Ile Leu Thr

115 120 125

ggt tat ggc tgg ttc gac ccc tgg ggc cag gga acc ctg gtc acc gtc 432

Gly Tyr Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val

130 135 140

tcc tca ggt ggt ggt ggt tcc ggt ggt ggt ggt tcc ggt ggt ggc gga 480

1 3 1 / 1 4 1

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
145 150 155 160

tcg gac atc gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg 528  
Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu  
165 170 175

ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac 576  
Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr  
180 185 190

agc tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga 624  
Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly  
195 200 205

cag cct cct aaa ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg 672  
Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly  
210 215 220

gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc 720  
Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu  
225 230 235 240

acc atc agc acc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag 768  
Thr Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln  
245 250 255

caa tat tat agt act cct ccg acg ttc ggc caa ggg acc aag gtg gaa 816  
Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu  
260 265 270

atc aaa cgt cgt gaa ttc gac tac aag gat gac gac gat aag tga 861  
Ile Lys Arg Arg Glu Phe Asp Tyr Lys Asp Asp Asp Asp Lys  
275 280 285

1 3 2 / 1 4 1

<210> 184

<211> 286

<212> PRT

<213> Homo sapiens

<400> 184

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala  
1 5 10 15

Ala Gln Pro Ala Met Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly  
20 25 30

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala  
35 40 45

Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala  
50 55 60

Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly  
65 70 75 80

Gly Thr Lys Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg  
85 90 95

Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser  
100 105 110

Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Asp Ile Leu Thr  
115 120 125

Gly Tyr Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val  
130 135 140

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
145 150 155 160

1 3 3 / 1 4 1

Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu  
165 170 175

Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr  
180 185 190

Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly  
195 200 205

Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly  
210 215 220

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu  
225 230 235 240

Thr Ile Ser Thr Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln  
245 250 255

Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu  
260 265 270

Ile Lys Arg Arg Glu Phe Asp Tyr Lys Asp Asp Asp Asp Lys  
275 280 285

<210> 185

<211> 846

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (846)

<223>

<400> 185

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Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala  
1 5 10 15

gcc cag ccg gcg atg gcc atg gcc cag gtg cag ctg gtg cag tct ggg 96  
Ala Gln Pro Ala Met Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly  
20 25 30

gct gag gtg aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gct 144  
Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala  
35 40 45

tct gga tac acc ttc acc ggc tac tat atg cac tgg gtg cga cag gcc 192  
Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala  
50 55 60

cct gga caa ggg ctt gag tgg atg gga tgg atc aac cct aac agt ggt 240  
Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly  
65 70 75 80

ggc aca aag tat gca cag aag ttt cag ggc agg gtc acc atg acc agg 288  
Gly Thr Lys Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg  
85 90 95

gac acg tcc atc agc aca gcc tac atg gag ctg agc agg ctg aga tct 336  
Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser  
100 105 110

gac gac acg gcc gtg tat tac tgt gcg aga gga tac gat att ttg act 384  
Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Asp Ile Leu Thr  
115 120 125

ggt tat ggc tgg ttc gac ccc tgg ggc cag gga acc ctg gtc acc gtc 432  
Gly Tyr Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val  
130 135 140

$$1\ 3\ 5 / 1\ 4\ 1$$

tcc tca ggt ggt ggt ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga	480
Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	
145 150 155 160	
tcg gaa att gtg ctg act cag tct cca ggc acc ctg tct ttg tct cca	528
Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro	
165 170 175	
ggg gaa aga gcc acc ctc tcc tgc aag gcc agt cag agt ttt agc agc	576
Gly Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser Phe Ser Ser	
180 185 190	
aac tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctg	624
Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu	
195 200 205	
ctc atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc	672
Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe	
210 215 220	
agt ggc agt aaa tct ggg aca gac ttc act ctc acc atc agc aga ctg	720
Ser Gly Ser Lys Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu	
225 230 235 240	
gag cct gaa gat ttt gca gtg tat tac tgt cag cag tat gtt acc tca	768
Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Thr Ser	
245 250 255	
ccg tac act ttt ggc cag ggg acc aag gtg gag atc aaa cgt cgt gaa	816
Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Arg Glu	
260 265 270	
ttc gac tac aag gat gac gac gat aag tga	846
Phe Asp Tyr Lys Asp Asp Asp Asp Lys	
275 280	

1 3 6 / 1 4 1

<210> 186

<211> 281

<212> PRT

<213> Homo sapiens

<400> 186

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala  
1 5 10 15

Ala Gln Pro Ala Met Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly  
20 25 30

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala  
35 40 45

Ser Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala  
50 55 60

Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly  
65 70 75 80

Gly Thr Lys Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg  
85 90 95

Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser  
100 105 110

Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Asp Ile Leu Thr  
115 120 125

Gly Tyr Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val  
130 135 140

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
145 150 155 160



1 3 7 / 1 4 1

Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro

165

170

175

Gly Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser Phe Ser Ser

180

185

190

Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu

195

200

205

Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe

210

215

220

Ser Gly Ser Lys Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu

225

230

235

240

Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Thr Ser

245

250

255

Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Arg Glu

260

265

270

Phe Asp Tyr Lys Asp Asp Asp Lys

275

280

<210> 187

<211> 852

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (852)

<223>

1 3 8 / 1 4 1

<400> 187

atg aaa tac ctg ctg ccg acc gct gct gct ggt ctg ctg ctc ctc gct 48  
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala  
1 5 10 15

gcc cag ccg gcg atg gcc atg gcc cag gtc cag ctg gtg caa tct ggg 96  
Ala Gln Pro Ala Met Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly  
20 25 30

gga ggc ttg gtc cag cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc 144  
Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala  
35 40 45

tct gga ttc acc ttt agt agc tat tgg atg agt tgg gtc cgc cag gct 192  
Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val Arg Gln Ala  
50 55 60

cca ggg aag ggg ctg gag tgg gtg gcc aac ata aag caa gat gga agt 240  
Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile Lys Gln Asp Gly Ser  
65 70 75 80

gag aaa tac tat gtg gac tct gtg aag ggc cga ttc acc atc tcc aga 288  
Glu Lys Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg  
85 90 95

gac aac gcc aag aac tca ctg tat ctg caa atg aac acc ctg aga gcc 336  
Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala  
100 105 110

gag gac acg gct gtg tat tac tgt gcg aga gat cgt ttg tgg acc cag 384  
Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Leu Trp Thr Gln  
115 120 125

ggg ttt ttt gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tca 432  
Gly Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
130 135 140

1 3 9 / 1 4 1

ggc gga tgc gac	480
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp	
145 150 155 160	
atc gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc gag	528
Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu	
165 170 175	
agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc tcc	576
Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser	
180 185 190	
aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag cct	624
Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro	
195 200 205	
cct aac ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc cct	672
Pro Asn Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro	
210 215 220	
gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc atc	720
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile	
225 230 235 240	
agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa tat	768
Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr	
245 250 255	
tat act act ccg tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa	816
Tyr Thr Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
260 265 270	
cgt gaa ttc gac tac aag gat gac gac gat aag tga	852
Arg Glu Phe Asp Tyr Lys Asp Asp Asp Asp Lys	
275 280	

1 4 0 / 1 4 1

<210> 188  
<211> 283  
<212> PRT  
<213> Homo sapiens

<400> 188

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala  
1 5 10 15

Ala Gln Pro Ala Met Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly  
20 25 30

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala  
35 40 45

Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val Arg Gln Ala  
50 55 60

Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile Lys Gln Asp Gly Ser  
65 70 75 80

Glu Lys Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg  
85 90 95

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala  
100 105 110

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Leu Trp Thr Gln  
115 120 125

Gly Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
130 135 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp

1 4 1 / 1 4 1

145                      150                      155                      160

Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu  
                    165                      170                      175

Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser  
                    180                      185                      190

Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro  
                    195                      200                      205

Pro Asn Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro  
                    210                      215                      220

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile  
225                      230                      235                      240

Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr  
                    245                      250                      255

Tyr Thr Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
                    260                      265                      270

Arg Glu Phe Asp Tyr Lys Asp Asp Asp Asp Lys  
                    275                      280